Access DB# ~~133~~ 135523

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: JANE ZARA Examiner #: 77512 Date: 10/19/04
Art Unit: 1635 Phone Number 30 2-0765 Serial Number: 09/802,376
Mail Box and Bldg/Room Location: 2028 Results Format Preferred (circle): PAPER DISK E-MAIL
2C18

If more than one search is submitted, please prioritize searches in order of need.

****

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims and abstract

Title of Invention: IN Formulations

Inventors (please provide full names): Van Nest et al. CRTC

Earliest Priority Filing Date: 3/9/01

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Please search Seq ID No: 1

— No size limit

— size limit to 100 NTS

Please include interference search.

1-22 ak

****

STAFF USE ONLY	Type of Search		Vendors and cost where applicable	
Searcher: Beverly C 25	NA Sequence (#)		STN	✓
Searcher Phone #:	AA Sequence (#)		Dialog	
Searcher Location:	Structure (#)		Questel/Orbit	
Date Searcher Picked Up:	Bibliographic		Dr.Link	
Date Completed:	Litigation		Lexis/Nexis	
Searcher Prep & Review Time:	Fulltext		Sequence Systems	
Clerical Prep Time:	Patent Family		WWW/Internet	
Online Time:	Other		Other (specify)	CGN

PTO-1590 (8-01)

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 28, 2005, 21:03:51 ; Search time 269 Seconds
(without alignments)
484.142 Million cell updates/sec

Title: US-09-802-376-1
Perfect score: 22
Sequence: 1 tgactgtgaacgttcgagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
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7: geneseqn2002bs:*
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11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	22	100.0	22	2	AAV32079	Aav32079 Nucleotid
2	22	100.0	22	2	AAV80097	Aav80097 Immunomod
3	22	100.0	22	2	AAV80103	Aav80103 Immunomod
4	22	100.0	22	2	AAV80102	Aav80102 Immunomod
5	22	100.0	22	2	AAX36624	Aax36624 ISS-ODN D
6	22	100.0	22	3	AAA14467	Aaa14467 Immunosti
7	22	100.0	22	3	AAA38072	Aaa38072 Immunosti
8	22	100.0	22	3	AAA38071	Aaa38071 Immunosti
9	22	100.0	22	3	AAA38065	Aaa38065 Immunosti
10	22	100.0	22	3	AAA90458	Aaa90458 CpG adjuv
11	22	100.0	22	3	AAA96253	Aaa96253 Sequence
12	22	100.0	22	3	AAZ55876	Aaz55876 Immunomod
13	22	100.0	22	3	AAC64051	Aac64051 Immunosti
14	22	100.0	22	4	AAH20403	Aah20403 CpG motif
15	22	100.0	22	4	AAH43338	Aah43338 Immunomod
16	22	100.0	22	4	AAH73439	Aah73439 Immunomod
17	22	100.0	22	4	AAH75992	Aah75992 Immunomod
18	22	100.0	22	4	AAF77040	Aaf77040 Immunomod
19	22	100.0	22	4	AAF29800	Aaf29800 Cholera t
20	22	100.0	22	4	AAH44109	Aah44109 5' termin
21	22	100.0	22	4	AAC82107	Aac82107 Oligonucl
22	22	100.0	22	4	AAA92377	Aaa92377 CG motif
23	22	100.0	22	4	AAH42533	Aah42533 Phosphoro
24	22	100.0	22	5	AAH41573	Aah41573 Immunosti
25	22	100.0	22	5	AAS14664	Aas14664 Immunosti
26	22	100.0	22	6	ABQ78627	Abq78627 ISS enhan
27	22	100.0	22	6	AAS15592	Aas15592 Immunosti
28	22	100.0	22	6	ABA03833	Aba03833 Immunosti
29	22	100.0	22	6	ABA03844	Aba03844 Immunosti
30	22	100.0	22	6	AAS16337	Aas16337 ISS polyn
31	22	100.0	22	6	AAD24885	Aad24885 Immunosti
32	22	100.0	22	6	AAD21877	Aad21877 Immunosti
33	22	100.0	22	6	ABQ75259	Abq75259 ISS immun
34	22	100.0	22	6	ABQ75153	Abq75153 ISS immun
35	22	100.0	22	6	ABQ75206	Abq75206 ISS immun
36	22	100.0	22	6	ABV73190	Abv73190 Nucleotid
37	22	100.0	22	6	AAS16348	Aas16348 ISS polyn
38	22	100.0	22	6	AAL44504	Aal44504 CpG motif
39	22	100.0	22	6	ABA03856	Aba03856 Immunosti
40	22	100.0	22	8	ABZ57964	Abz57964 Immunosti
41	22	100.0	22	8	ABZ77582	Abz77582 Nucleotid
42	22	100.0	22	9	ADB88931	Adb88931 Chimeric
43	22	100.0	22	9	ADB88799	Adb88799 Chimeric
44	22	100.0	22	9	ADB88821	Adb88821 Chimeric
45	22	100.0	22	9	ADB88876	Adb88876 Chimeric

ALIGNMENTS

RESULT 1
AAV32079
ID AAV32079 standard; DNA; 22 BP.
XX
AC AAV32079;
XX
DT 09-SEP-1998 (first entry)
XX
DE Nucleotide sequence of DY1018.
XX
KW DY1018; beta-gal; ISS-PN/IMM; antigen; immune response; antibody;
KW immunisation; anaphylaxis; IgE; retinopathies; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .22
FT /*tag= a
FT /note= "phosphothioate backbone"
XX
PN WO9816247-A1.
XX
PD 23-APR-1998.
XX
PF 09-OCT-1997; 97WO-US019004.
XX
PR 11-OCT-1996; 96US-0028118P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Carson DA, Raz E, Roman M;
XX
DR WPI; 1998-261028/23.
XX
PT New immunomodulatory compositions - comprising an antigen conjugated to a
PT polynucleotide that contains an immunostimulatory sequence.
XX
PS Example 1; Page 36; 69pp; English.
XX
CC This is the nucleotide sequence of DY1018, which is conjugated to beta-
CC gal to form ISS-PN/IMM, comprising an immunomodulatory molecule (IMM),
CC which comprises an antigen conjugated to a polynucleotide (PN) that
CC contains at least one immunostimulatory nucleotide sequence (ISS). The

CC conjugate synergistically boost the magnitude of the host immune response
CC against an antigen to a level greater that the host immune response to
CC either the IMM, antigen or ISS-PN alone. These responses to ISS-PN/IMM
CC conjugates are particularly acute during the important early phase of the
CC host immune response to an antigen. The ISS-PN/IMM conjugates boost both
CC humoral (antibody) and cellular (Th1 type) immune responses of the host.
CC Thus, use of the method to boost the immune responsiveness of a host to
CC subsequent challenge by a sensitising antigen without immunisation avoids
CC the risk of Th2-mediated, immunisation-induced anaphylaxis by suppressing
CC IgE production in response to the antigen challenge. The conjugates can
CC also be used to combat pathogenic infection and to stimulate therapeutic
CC angiogenesis to treat conditions in which localised blood flow plays a
CC significant etiological role, e.g. retinopathies
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||||||||||||||
Db 1 TGACTGTGAACGTTCGAGATGA 22

RESULT 2
AAV80097
ID AAV80097 standard; DNA; 22 BP.
XX
AC AAV80097;
XX
DT 12-MAR-1999 (first entry)
XX
DE Immunomodulatory oligo comprising an ISS sequence.
XX
KW Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.
XX
OS Synthetic.
XX
PN WO9855495-A2.
XX
PD 10-DEC-1998.
XX
PF 05-JUN-1998; 98WO-US011578.
XX
PR 06-JUN-1997; 97US-0048793P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Schwartz D, Roman M, Dina D;
XX
DR WPI; 1999-059898/05.
XX
PT Immunostimulatory oligonucleotides regulate the immune system - and
PT contain an immune-stimulating octanucleotide sequence; for treating
PT cancer, allergic and infectious diseases.
XX
PS Claim 5; Page 29; 63pp; English.
XX
CC The invention relates to immunomodulatory oligonucleotides that comprise
CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
CC sequences are selected from the group consisting of AACGTTCC, AACGTTCG,
CC GACGTTCC, and GACGTTCG. The immunomodulatory sequences are used to treat
CC patients needing immune regulation, such as those suffering from cancer,
CC an allergic disease and asthma. They are also used to prevent infectious
CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
CC Schistosoma. The immunomodulatory sequences are used to screen for human
CC immunostimulatory activity by incubating macrophage cells and the
CC oligonucleotide; and determining the relative amount of Th1-biased
CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
CC specific claimed examples of such immunomodulatory oligonucleotides
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||||||||||||||
Db 1 TGACTGTGAACGTTCGAGATGA 22

RESULT 3
AAV80103
ID AAV80103 standard; DNA; 22 BP.
XX
AC AAV80103;
XX
DT 12-MAR-1999 (first entry)
XX
DE Immunomodulatory oligo comprising an ISS sequence.
XX
KW Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 11
FT /*tag= a
FT /note= "5-bromocytosine"
XX
PN WO9855495-A2.
XX
PD 10-DEC-1998.
XX
PF 05-JUN-1998; 98WO-US011578.
XX
PR 06-JUN-1997; 97US-0048793P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Schwartz D, Roman M, Dina D;
XX
DR WPI; 1999-059898/05.
XX
PT Immunostimulatory oligonucleotides regulate the immune system - and
PT contain an immune-stimulating octanucleotide sequence; for treating
PT cancer, allergic and infectious diseases.
XX
PS Claim 24; Page 30; 63pp; English.
XX
CC The invention relates to immunomodulatory oligonucleotides that comprise
CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
CC sequences are selected from the group consisting of AACGTTCC, AACGTTCG,
CC GACGTTCC, and GACGTTCG. The immunomodulatory sequences are used to treat
CC patients needing immune regulation, such as those suffering from cancer,
CC an allergic disease and asthma. They are also used to prevent infectious
CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
CC Schistosoma. The immunomodulatory sequences are used to screen for human
CC immunostimulatory activity by incubating macrophage cells and the
CC oligonucleotide; and determining the relative amount of Th1-biased
CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
CC specific claimed examples of such immunomodulatory oligonucleotides
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

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  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22
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RESULT 4
AAV80102
ID AAV80102 standard; DNA; 22 BP.
XX
AC AAV80102;
XX
DT 12-MAR-1999 (first entry)
XX
DE Immunomodulatory oligo comprising an ISS sequence.
XX
KW Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 11
FT /*tag= a
FT /note= "5-bromocytosine"
XX
PN WO9855495-A2.
XX
PD 10-DEC-1998.
XX
PF 05-JUN-1998; 98WO-US011578.
XX
PR 06-JUN-1997; 97US-0048793P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Schwartz D, Roman M, Dina D;
XX
DR WPI; 1999-059898/05.
XX
PT Immunostimulatory oligonucleotides regulate the immune system - and
PT contain an immune-stimulating octanucleotide sequence; for treating
PT cancer, allergic and infectious diseases.
XX
PS Claim 23; Page 30; 63pp; English.
XX
CC The invention relates to immunomodulatory oligonucleotides that comprise
CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
CC sequences are selected from the group consisting of AACGTTCC, AACGTTCG,
CC GACGTTCC, and GACGTTCG. The immunomodulatory sequences are used to treat
CC patients needing immune regulation, such as those suffering from cancer,
CC an allergic disease and asthma. They are also used to prevent infectious
CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
CC Schistosoma. The immunomodulatory sequences are used to screen for human
CC immunostimulatory activity by incubating macrophage cells and the
CC oligonucleotide; and determining the relative amount of Th1-biased
CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
CC specific claimed examples of such immunomodulatory oligonucleotides
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

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  Query Match            100.0%;  Score 22;  DB 2;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.24;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22
```

RESULT 5
AAX36624
ID AAX36624 standard; DNA; 22 BP.
XX
AC AAX36624;
XX
DT 09-JUL-1999 (first entry)
XX
DE ISS-ODN DY1018 nucleotide sequence.
XX
KW Antigen-stimulated inflammation; immunostimulatory oligonucleotide;
KW granulocyte-mediated tissue inflammation; Th2 type immune response;
KW immune responsiveness modulation; idiopathic hypereosiniphilic syndrome;
KW cutaneous basophil hypersensitivity; ISS-ODN; asthma; nasal polyposis;
KW allergic rhinitis; atopic dermatitis; allergic conjunctivitis;
KW eosinophilic fasciitis; therapy; ss.
XX
OS Synthetic.
XX
PN WO9911275-A2.
XX
PD 11-MAR-1999.
XX
PF 04-SEP-1998; 98WO-US018382.
XX
PR 05-SEP-1997; 97US-00927120.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Ray E;
XX
DR WPI; 1999-312404/26.
XX
PT Reducing antigen-stimulated granulocyte-mediated inflammation.
XX
PS Example 2; Page 30; 69pp; English.
XX
CC This is the ISS-ODN DY1018 nucleotide sequence. The invention relates to
CC a method for preventing or reducing antigen-stimulated, granulocyte-
CC mediated tissue inflammation in a mammal, by administering an
CC immunostimulatory oligonucleotide (ISS-ODN), where: (a) reduction in, or
CC the absence of, a Th2 type immune response is measured; or (b) there is a
CC reduction or absence of other clinical signs of inflammation in the host
CC after antigen challenge. The method is used to reduce or suppress
CC granulocyte-mediated inflammation in a host tissue, and to modulate the
CC host's immune responsiveness to an antigen, particularly where the
CC subject suffers from asthma, nasal polyposis, allergic rhinitis, atopic
CC dermatitis, allergic conjunctivitis, eosinophilic fasciitis, idiopathic
CC hypereosiniphilic syndrome, or cutaneous basophil hypersensitivity.
CC Unlike prior art treatment by antigen immunisation, the method is an
CC antigen-independent method, and avoids host production of both
CC interleukin-4 (IL-4), which carries risk of anaphylaxis, and IL-5 which
CC actually encourages granulocyte adhesion to endothelia
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

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Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22
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RESULT 6
AAA14467
ID AAA14467 standard; DNA; 22 BP.

XX
AC AAA14467;
XX
DT 21-AUG-2000 (first entry)
XX
DE Immunostimulatory oligonucleotide (ISS-ODN) DY1018.
XX
KW Immunostimulatory oligonucleotide; adjuvant; mucosal immunity;
KW secretory immunoglobulin A production; sIgA; Th1 phenotype; ds.
XX
OS Synthetic.
XX
PN WO200020039-A1.
XX
PD 13-APR-2000.
XX
PF 15-SEP-1999; 99WO-US021203.
XX
PR 05-OCT-1998; 98US-00167039.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Raz E, Horner AA, Carson DA;
XX
DR WPI; 2000-303647/26.
XX
PT Immunostimulatory oligonucleotide adjuvant induces mucosal immunity to an
PT antigen in a mammalian host through production of secretory
PT immunoglobulin A.
XX
PS Claim 8; Page 21; 64pp; English.
XX
CC The invention relates to a method of inducing mucosal immunity to an
CC antigen in a mammalian host, including the the production of secretory
CC immunoglobulin A (sIgA). Immune protection in the mucosa (the principal
CC site of entry of most foreign antigens) is mediated by mucosa-associated
CC lymphoid tissue, epithelial and distinct B-cell, T-cell and accessory
CC cell sub-populations. The primary immune response which characterises the
CC induction of mucosal immunity to an antigen is sIgA production by
CC activated B-cells. The method comprises introducing an immunostimulatory
CC oligonucleotide (ISS-ODN) and the antigen into host mucosa, where the ISS
CC -ODN includes a core nucleotide sequence. The core nucleotide sequence is
CC 5'-Purine-Purine-C-G-Pyrimidine-Pyrimidine-3', specific examples of which
CC are AACGTT, AGCGTC and GACGTT (SEQ ID NOs 1-3). A specific example of an
CC ISS-ODN is DY1018 (AAA14467). The ISS-ODN is used as an adjuvant with an
CC antigen for stimulating mucosal immunity. The level of sIgA production
CC induced in the host is at least 3 times the magnitude of sIgA production
CC achievable in response to introduction of antigen alone into the mucosal
CC tissue and is equivalent or greater than the magnitude of sIgA production
CC achievable in response to introduction of the antigen and cholera toxin
CC adjuvant into the mucosal tissue. The host immune response is stimulated
CC to antigen specific IgA production, biased towards the Th1 phenotype
CC while antigen-induced IgE production is avoided. The adjuvant has little
CC or no known toxicity in mammals and its efficacy is comparable to that of
CC cholera toxin which is used as a mucosal adjuvant. The present sequence
CC represents the immunostimulatory oligonucleotide DY1018
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||||||||||||||
Db 1 TGACTGTGAACGTTCGAGATGA 22

RESULT 7
AAA38072
ID AAA38072 standard; DNA; 22 BP.
XX
AC AAA38072;
XX
DT 24-AUG-2000 (first entry)
XX
DE Immunostimulatory sequence (ISS) #7.
XX
KW Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;
KW gp120; human immunodeficiency virus; HIV; immune response; infection;
KW development; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
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FT /note= "5-Bromocytosine"
XX
PN WO200021556-A1.
XX
PD 20-APR-2000.
XX
PF 08-OCT-1999; 99WO-US023677.
XX
PR 09-OCT-1998; 98US-0103733P.
PR 07-OCT-1999; 99US-00415186.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Tighe H, Raz E, Schwartz D, Takabayashi K;
XX
DR WPI; 2000-317846/27.
XX
PT Anti-HIV composition comprises immunostimulatory polynucleotides and HIV
PT glycoprotein gp120 useful for modulating, stimulating an immune response
PT against HIV in an HIV infected individual.
XX
PS Disclosure; Page 17; 65pp; English.
XX
CC The present invention relates to an immunostimulatory composition
CC comprising a human immunodeficiency virus (HIV) antigen, and an
CC immunomodulatory polynucleotide comprising an immunostimulatory sequence
CC (ISS). This sequence represents an ISS that can be used in the
CC composition. An immunostimulatory composition which comprises a gp120
CC conjugated to an immunomodulatory polynucleotide, or is proximately
CC associated to it and not conjugated, is used for modulating or
CC stimulating a specific immune response against gp120 in an individual by
CC producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It
CC is also used for suppressing or delaying development of HIV infection in
CC an individual infected with HIV or an individual at risk of infection
CC with HIV, respectively. It is also used for treating an individual
CC infected with HIV in need of immune modulation
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||||||||||||||
Db 1 TGACTGTGAACGTTCGAGATGA 22

RESULT 8
AAA38071
ID AAA38071 standard; DNA; 22 BP.
XX
AC AAA38071;
XX

```
DT   24-AUG-2000  (first entry)
XX
DE   Immunostimulatory sequence (ISS) #7.
XX
KW   Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;
KW   gp120; human immunodeficiency virus; HIV; immune response; infection;
KW   development; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
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FT                   /mod_base= OTHER
FT                   /note= "5-Bromocytosine"
XX
PN   WO200021556-A1.
XX
PD   20-APR-2000.
XX
PF   08-OCT-1999;   99WO-US023677.
XX
PR   09-OCT-1998;   98US-0103733P.
PR   07-OCT-1999;   99US-00415186.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Tighe H,  Raz E,  Schwartz D,  Takabayashi K;
XX
DR   WPI; 2000-317846/27.
XX
PT   Anti-HIV composition comprises immunostimulatory polynucleotides and HIV
PT   glycoprotein gp120 useful for modulating, stimulating an immune response
PT   against HIV in an HIV infected individual.
XX
PS   Disclosure; Page 17; 65pp; English.
XX
CC   The present invention relates to an immunostimulatory composition
CC   comprising a human immunodeficiency virus (HIV) antigen, and an
CC   immunomodulatory polynucleotide comprising an immunostimulatory sequence
CC   (ISS). This sequence represents an ISS that can be used in the
CC   composition. An immunostimulatory composition which comprises a gp120
CC   conjugated to an immunomodulatory polynucleotide, or is proximately
CC   associated to it and not conjugated, is used for modulating or
CC   stimulating a specific immune response against gp120 in an individual by
CC   producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It
CC   is also used for suppressing or delaying development of HIV infection in
CC   an individual infected with HIV or an individual at risk of infection
CC   with HIV, respectively. It is also used for treating an individual
CC   infected with HIV in need of immune modulation
XX
SQ   Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 22;  DB 3;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.24;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 9
AAA38065
ID   AAA38065 standard; DNA; 22 BP.
XX
AC   AAA38065;
XX
DT   24-AUG-2000  (first entry)
XX
DE   Immunostimulatory sequence (ISS) #1.
XX
KW   Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;
KW   gp120; human immunodeficiency virus; HIV; immune response; infection;
KW   development; ss.
XX
OS   Synthetic.
XX
PN   WO200021556-A1.
XX
PD   20-APR-2000.
XX
PF   08-OCT-1999;   99WO-US023677.
XX
PR   09-OCT-1998;   98US-0103733P.
PR   07-OCT-1999;   99US-00415186.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Tighe H,  Raz E,  Schwartz D,  Takabayashi K;
XX
DR   WPI; 2000-317846/27.
XX
PT   Anti-HIV composition comprises immunostimulatory polynucleotides and HIV
PT   glycoprotein gp120 useful for modulating, stimulating an immune response
PT   against HIV in an HIV infected individual.
XX
PS   Claim 3; Page 16; 65pp; English.
XX
CC   The present invention relates to an immunostimulatory composition
CC   comprising a human immunodeficiency virus (HIV) antigen, and an
CC   immunomodulatory polynucleotide comprising an immunostimulatory sequence
CC   (ISS). This sequence represents an ISS that can be used in the
CC   composition. An immunostimulatory composition which comprises a gp120
CC   conjugated to an immunomodulatory polynucleotide, or is proximately
CC   associated to it and not conjugated, is used for modulating or
CC   stimulating a specific immune response against gp120 in an individual by
CC   producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It
CC   is also used for suppressing or delaying development of HIV infection in
CC   an individual infected with HIV or an individual at risk of infection
CC   with HIV, respectively. It is also used for treating an individual
CC   infected with HIV in need of immune modulation
XX
SQ   Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 22;  DB 3;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.24;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 10
AAA90458
ID   AAA90458 standard; DNA; 22 BP.
XX
AC   AAA90458;
XX
DT   10-JAN-2001  (first entry)
XX
DE   CpG adjuvant oligonucleotide, SEQ ID NO:19.
XX
KW   CpG oligonucleotide; CpG motif; adjuvant; microdroplet emulsion;
KW   microemulsion; adsorbent microparticle; vaccine; Th1 immune response;
KW   viral infection; bacterial infection; parasitic infection; HCV; HBV;
KW   hepatitis C virus; hepatitis B virus; herpes simplex virus; HSV; HIV;
KW   human immunodeficiency virus; cytomegalovirus; CMV; influenza virus;
KW   rabies virus; cholera; diphtheria; tetanus; pertussis;
KW   Helicobacter pylori; Haemophilus influenzae; malaria; ss.
XX
OS   Synthetic.
XX
PN   WO200050006-A2.
XX
```

PD 31-AUG-2000.
XX
PF 09-FEB-2000; 2000WO-US003331.
XX
PR 26-FEB-1999; 99US-0121858P.
PR 29-JUL-1999; 99US-0146391P.
PR 28-OCT-1999; 99US-0161997P.
XX
PA (CHIR) CHIRON CORP.
XX
PI O'hagan D, Ott GS, Donnelly J, Kazzaz J, Ugozzoli M, Singh M;
PI Barackman J;
XX
DR WPI; 2000-587123/55.
XX
PT Microemulsion having an adsorbent surface comprising a microdroplet
PT emulsion consisting of a metabolizable oil and an emulsifying agent which
PT is a detergent, useful as a vaccine to treat bacterial, viral, and
PT parasitic infection.
XX
PS Claim 17; Page 40; 95pp; English.
XX
CC The invention relates to a microdroplet emulsion (microemulsion) with an
CC adsorbent surface, and which comprises a metabolisable oil and an
CC emulsifying agent (a detergent). It also relates to a composition
CC comprising the microemulsion and a microparticle with an adsorbent
CC surface, where the microparticle comprises a polymer selected from a
CC poly(alpha-hydroxy acid), a polyhydroxy butyric acid, a polycaprolactone,
CC a polyorthoester, a polyanhydride, and a polycyanoacrylate, and a second
CC detergent. The surface of the microparticles efficiently adsorb
CC biologically active macromolecules such as DNA, polypeptides, antigens,
CC hormones, pharmaceuticals, enzymes, mediators of transcription or
CC translation, metabolic intermediates and adjuvants. Additionally, a
CC second biologically active molecule may be encapsulated within the
CC microparticle. The microemulsion can be used in methods of immunising a
CC host animal, particularly a human, against a viral, bacterial or
CC parasitic infection, and in methods of increasing a Th1 immune response.
CC The microemulsions (having the appropriate antigens adsorbed) may be
CC particularly used as vaccines for hepatitis C virus (HCV), hepatitis B
CC virus (HBV), herpes simplex virus (HSV), human immunodeficiency virus
CC (HIV), cytomegalovirus (CMV), influenza virus, and rabies virus; the
CC bacteria which cause cholera, diphtheria, tetanus and pertussis;
CC Helicobacter pylori and Haemophilus influenzae; and malaria-causing
CC parasites. Sequences AAA90447-A90467 represent Th1 lymphocyte stimulating
CC oligonucleotides containing at least one CpG motif which are claimed for
CC use as adjuvants in the compositions of the invention
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||||||||||||||
Db 1 TGACTGTGAACGTTCGAGATGA 22

RESULT 11
AAA96253
ID AAA96253 standard; DNA; 22 BP.
XX
AC AAA96253;
XX
DT 08-FEB-2001 (first entry)
XX
DE Sequence of a stabilised oligonucleotide with antitumour activity.
XX
KW Antitumour; immunostimulatory oligonucleotide; tumour; anaplasia;
KW glioblastoma; medullablastoma; neuroblastoma; melanoma; carcinoma; ss.
XX
OS Synthetic.
XX
PN WO200056342-A2.
XX
PD 28-SEP-2000.
XX
PF 17-MAR-2000; 2000WO-FR000676.
XX
PR 19-MAR-1999; 99FR-00003433.
XX
PA (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
PA (INRM) INST NAT SANTE & RECH MEDICALE.
XX
PI Carpentier A;
XX
DR WPI; 2000-602192/57.
XX
PT Use of stabilized oligonucleotides as antitumor agents, particularly
PT against nervous system tumors, have optimal activity and are not toxic.
XX
PS Example 2; Page 16; 57pp; French.
XX
CC The present sequence represents a stabilised oligonucleotide which has
CC antitumour activity. The oligonucleotide comprises an octomer motif of
CC the type 5'-purine-purine-CG-pyrimidine-pyrimidine-X-X-3', where the pair
CC X-X is AT, AA, CT or TT. The oligonucleotides are immunostimulatory, and
CC are not toxic. They may be adapted for use in animals or humans. The
CC stabilised oligonucleotides are used for treating tumours, of any type
CC and any degree of anaplasia, particularly human tumours in the peripheral
CC or central nervous systems, specifically glioblastomas, medullablastomas,
CC neuroblastomas, melanomas or carcinomas
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||||||||||||||
Db 1 TGACTGTGAACGTTCGAGATGA 22

RESULT 12
AAZ55876
ID AAZ55876 standard; DNA; 22 BP.
XX
AC AAZ55876;
XX
DT 10-APR-2000 (first entry)
XX
DE Immunomodulatory oligonucleotide SEQ ID NO: 1.
XX
KW Immunomodulation; immunostimulatory sequence; adjuvant;
KW Th1 immune response; cytotoxic T-cell; cytokine; cancer; allergy; asthma;
KW immunocontraception; ss.
XX
OS Mus musculus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .22
FT /*tag= a
FT /note= "Phosphorothioate linkages"
FT misc_feature 9. .16
FT /*tag= b
FT /note= "Immunostimulatory sequence (ISS)"
XX
PN WO9962923-A2.
XX
PD 09-DEC-1999.
XX
PF 04-JUN-1999; 99WO-US012538.
XX
PR 05-JUN-1998; 98US-0088310P.

PR 01-JUN-1999; 99US-00324191.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Schwartz D;
XX
DR WPI; 2000-105687/09.
XX
PT Novel immunomodulatory oligonucleotide used to induce a Th1-type immune
PT response, e.g. to tumor antigens.
XX
PS Example 1; Page 35; 54pp; English.
XX
CC Sequences AAZ55876-Z55877 and AAZ55880-Z55886 represent immunomodulatory
CC oligonucleotides comprising an immunostimulatory sequence (ISS, e.g.,
CC AACGTC, AACGTT, AGCGTC, AGCGCT, AGCGTT, GACGTC, GACGTT, GGCGTT, AACGTTCC
CC and GACGTTCC). The invention relates to oligonucleotides comprising one
CC or more ISSs, where the ISS comprises at least one modified cytosine with
CC an electron-withdrawing moiety at position C-5 or C-6 of the base.
CC Sequences AAZ55877 and AAZ55880-Z55886 contain ISSs comprising at least
CC one bromocytosine, whereas sequence AAZ55876 contains an unmodified ISS.
CC The immunomodulatory oligonucleotides have an adjuvant-like effect; when
CC formulated with an antigen, the oligonucleotides stimulate production of
CC Th1-type cytokines, and induce a Th1-type immune response (activation of
CC cytotoxic T cells), while simultaneously downregulating the Th2-type
CC response. The Th1 response is particularly effective for control of
CC viruses and intracellular parasites. The immunomodulatory
CC oligonucleotides are used, particularly when formulated with an antigen
CC or a facilitator, for modulating immune responses. Such compositions may
CC be used in tumour therapy, in treatment of allergy (including asthma),
CC for inducing a vigorous cellular response (against a virus, bacterium,
CC fungus or protozoan), and also in contraceptive vaccines based on sperm
CC antigens
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||||||||||||||
Db 1 TGACTGTGAACGTTCGAGATGA 22

RESULT 13
AAC64051
ID AAC64051 standard; DNA; 22 BP.
XX
AC AAC64051;
XX
DT 15-FEB-2001 (first entry)
XX
DE Immunostimulatory CpG phosphorothioate oligodeoxynucleotide.
XX
KW CpG oligodeoxynucleotide; phosphorothioate; immunostimulatory; ISS ODN;
KW enhanced antigen presentation; antigen-presenting cell; APC;
KW T-cell activation; tumour cell; tumour antigen; cancer immunotherapy;
KW vaccine; ss.
XX
OS Synthetic.
XX
PN WO200062787-A1.
XX
PD 26-OCT-2000.
XX
PF 11-APR-2000; 2000WO-US009664.
XX
PR 15-APR-1999; 99US-00292278.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Raz E, Martin-Orozco E;
XX
DR WPI; 2000-679548/66.
XX
PT Enhancing antigen-presentation capabilities of T-cells for cancer
PT immunotherapy, by contacting cells with an immunostimulatory
PT oligonucleotide.
XX
PS Example I; Page 18; 42pp; English.
XX
CC The invention relates to a method of inducing activation of T-cells to
CC respond to an antigen, comprising contacting antigen-presenting cells
CC (APC) with an immunostimulatory oligodeoxynucleotide (ISS-ODN). The APCs
CC thus treated have enhanced antigen presenting capabilities compared to
CC antigen-activated APCs. APCs with enhanced antigen-presentation
CC capabilities then present the antigen to T-cells. The method is useful
CC for cancer immunotherapy. The ISS-ODN is used to enhance the tumour
CC antigen presenting capacity of tumour cells, thereby inducing T-cell
CC activation, and is therefore useful for treating tumours. Additionally,
CC tumour cells treated with an ISS-ODN ex vivo are useful as vaccines. ISS-
CC ODN treated APCs are induced to take up antigen through upregulation of
CC Fc-receptor expression, to present antigen through upregulation of major
CC histocompatibility complex (MHC) Class I and II expression and CD1d
CC expression, to produce co-stimulatory factors (B7 and CD40), to provide
CC cell-to-cell adhesion through upregulation of intercellular adhesion
CC molecule (ICAM) expression, and to increase Th1 stimulatory cytokine
CC production, all at levels greater than that achieved through contact of
CC APC with antigen alone. The present sequence represents a
CC phosphorothioate CpG ISS-ODN used in the exemplifications of the
CC invention
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||||||||||||||
Db 1 TGACTGTGAACGTTCGAGATGA 22

RESULT 14
AAH20403
ID AAH20403 standard; DNA; 22 BP.
XX
AC AAH20403;
XX
DT 03-AUG-2001 (first entry)
XX
DE CpG motif containing oligonucleotide SEQ ID #21.
XX
KW Immune system stimulator; CpG motif; CpG receptor; CpG-R; antibacterial;
KW immune response; vaccine adjuvant; tumour immunotherapy; allergy;
KW anti-inflammatory; cystic fibrosis; sepsis; heart disease; chlamydia;
KW inflammatory bowel disease; arthritis; multiple sclerosis; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 1. .22
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate internucleoside linkages"
XX
PN WO200132877-A2.
XX
PD 10-MAY-2001.
XX
PF 01-NOV-2000; 2000WO-US041735.
XX
PR 02-NOV-1999; 99US-0163157P.
PR 24-NOV-1999; 99US-0167389P.
XX

PA (CHIR) CHIRON CORP.
XX
PI Mackichan ML;
XX
DR WPI; 2001-343486/36.
XX
PT Novel CpG receptor and nucleic acid molecule encoding the receptor, for
PT modulating immune response and for identifying compounds of therapeutic
PT use which bind and/or modulate the activity of the receptor.
XX
PS Example 1; Page 14; 41pp; English.
XX
CC Unmethylated CG dinucleotide sequences are commonly found in bacterial
CC DNA, and have been found to stimulate the innate immune system. Natural
CC killer and T cells are activated by exposure to oligonucleotides
CC containing CpG motifs. Oligonucleotides containing CpG motifs can be used
CC as adjuvants in vaccines. The present invention relates to a CpG
CC receptor. The CpG receptor contains a Toll homology domain (THD). The
CC Toll receptor family are associated with responses to pathogens. CpG
CC oligonucleotides may act as stimulators of various immune responses. The
CC CpG receptor or cells expressing the receptor are useful for identifying
CC a compound which binds to or modulates an activity of the CpG receptor.
CC The compounds are useful in e.g. vaccine adjuvants promoting cell-
CC mediated immune responses, antibacterials, (e.g. protection from Listeria
CC infection), tumour immunotherapy, allergy treatment, (e.g. suppressing
CC IgE in human PBMC, shifting from Th2 to Th1) and as anti-inflammatory
CC agents (e.g. for use in cystic fibrosis, sepsis, heart disease,
CC chlamydia, inflammatory bowel disease, arthritis and multiple sclerosis).
CC The present sequence represents a CpG motif containing oligonucleotide
CC used in examples demonstrating that CpG oligonucleotides can activate the
CC MAPK pathways and NF-kappaB
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||||||||||||||
Db 1 TGACTGTGAACGTTCGAGATGA 22

RESULT 15
AAH43338
ID AAH43338 standard; DNA; 22 BP.
XX
AC AAH43338;
XX
DT 13-DEC-2001 (first entry)
XX
DE Immunomodulatory polynucleotide 1018.
XX
KW Immunomodulation; inflammation; gastrointestinal tract;
KW ulcerative colitis; Crohn's disease; inflammatory bowel disease;
KW diarrhoea; rectal bleeding; weight loss; colon; weight; lesion; ss.
XX
OS Synthetic.
XX
PN WO200162207-A2.
XX
PD 30-AUG-2001.
XX
PF 22-FEB-2001; 2001WO-US006034.
XX
PR 23-FEB-2000; 2000US-0184256P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Raz E, Rachmilewitz D;
XX
DR WPI; 2001-565393/63.
XX
PT Ameliorating gastrointestinal inflammation e.g. inflammatory bowel
PT disease involves administering an immunomodulatory nucleic acid.
XX
PS Claim 7; Page 28; 58pp; English.
XX
CC The sequences given in AAH43338-48 represent immunomodulatory
CC polynucleotides which may be used to ameliorate inflammation of the
CC gastrointestinal tract by administering a nucleic acid comprising one of
CC these sequences. These polynucleotides all comprise an immunomodulatory
CC nucleotide sequence of 5'-CpG-3' (I). The nucleotides may be used for
CC ameliorating or reducing gastrointestinal inflammation e.g. chronic or
CC acute gastrointestinal inflammation, ulcerative colitis, Crohn's disease
CC caused by inflammatory bowel disease; diarrhoea, rectal bleeding, weight
CC loss; to reduce colon weight and colon lesions; to reduce a colonic
CC inflammation. The immunomodulatory polynucleotides treat inflammatory
CC bowel disease satisfactorily and effectively and have little or no
CC toxicity even at a high dosage of 50000 micro-g. They also reduce the
CC risk of colonic cancer by treating ulcerative colitis
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||||||||||||||
Db 1 TGACTGTGAACGTTCGAGATGA 22

Search completed: March 28, 2005, 22:51:34
Job time : 274 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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Minimum DB seq length: 0
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	22	100.0	22	4	US-09-235-742-19	Sequence 19, Appl
	2	22	100.0	22	4	US-09-347-343-32	Sequence 32, Appl
	3	22	100.0	22	4	US-09-820-484-1	Sequence 1, Appli
	4	22	100.0	22	4	US-09-820-484-3	Sequence 3, Appli
	5	22	100.0	22	4	US-09-774-403A-1	Sequence 1, Appli
	6	22	100.0	22	4	US-09-296-477-2	Sequence 2, Appli
	7	22	100.0	22	4	US-09-308-036A-1	Sequence 1, Appli
	8	22	100.0	22	4	US-09-791-500-1	Sequence 1, Appli
	9	22	100.0	22	4	US-09-565-906-2	Sequence 2, Appli
	10	21	95.5	22	4	US-09-296-477-15	Sequence 15, Appl
	11	20.4	92.7	22	3	US-09-092-314-2	Sequence 2, Appli
	12	20.4	92.7	22	4	US-09-820-484-2	Sequence 2, Appli
	13	20.4	92.7	22	4	US-09-820-484-6	Sequence 6, Appli
	14	20.4	92.7	22	4	US-09-774-403A-2	Sequence 2, Appli
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	19	20.4	92.7	22	4	US-09-791-500-5	Sequence 5, Appli
	20	20.4	92.7	22	4	US-09-791-500-6	Sequence 6, Appli
	21	20	90.9	22	4	US-09-296-477-16	Sequence 16, Appl
	22	19.4	88.2	22	4	US-09-296-477-12	Sequence 12, Appl
	23	18.8	85.5	22	3	US-09-092-314-1	Sequence 1, Appli
	24	18.8	85.5	22	3	US-09-092-314-3	Sequence 3, Appli
	25	18.8	85.5	22	3	US-09-092-314-10	Sequence 10, Appl
	26	18.8	85.5	22	4	US-09-235-742-20	Sequence 20, Appl
	27	18.8	85.5	22	4	US-09-347-343-33	Sequence 33, Appl
	28	18.8	85.5	22	4	US-09-820-484-7	Sequence 7, Appli
	29	18.8	85.5	22	4	US-09-774-403A-3	Sequence 3, Appli
	30	18.8	85.5	22	4	US-09-296-477-3	Sequence 3, Appli
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	35	17.2	78.2	22	3	US-09-092-314-4	Sequence 4, Appli
	36	17.2	78.2	22	4	US-09-296-477-9	Sequence 9, Appli
	37	17.2	78.2	22	4	US-09-296-477-13	Sequence 13, Appl
	38	17.2	78.2	22	4	US-09-791-500-9	Sequence 9, Appli
	39	17.2	78.2	601	4	US-09-949-016-131826	Sequence 131826,
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	43	16.2	73.6	128723	4	US-09-949-016-17533	Sequence 17533, A
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ALIGNMENTS

RESULT 1
US-09-235-742-19
; Sequence 19, Application US/09235742
; Patent No. 6498148
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; TITLE OF INVENTION: Immunization-Free Methods for Treating
; TITLE OF INVENTION: Antigen-Stimulated Inflammation in a Mammalian Host and
; TITLE OF INVENTION: Shifting the Host's Antigen Immune Responsiveness to a TH1
; TITLE OF INVENTION: Phenotype
; FILE REFERENCE: 6510-170CON4
; CURRENT APPLICATION NUMBER: US/09/235,742
; CURRENT FILING DATE: 1999-01-21
; EARLIER APPLICATION NUMBER: 08/927,120
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 08/593,554
; EARLIER FILING DATE: 1996-01-30
; EARLIER APPLICATION NUMBER: 08/725,968
; EARLIER FILING DATE: 1996-10-04
; EARLIER APPLICATION NUMBER: 60/028,118
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant or Synthetic Sequence
US-09-235-742-19

Query Match 100.0%; Score 22; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22
```

RESULT 2
US-09-347-343-32
; Sequence 32, Application US/09347343A
; Patent No. 6514948
; GENERAL INFORMATION:
; APPLICANT: RAZ, Eyal R.
; APPLICANT: KOBAYASHI, Hiroko
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE
; FILE REFERENCE: 30448.64US01
; CURRENT APPLICATION NUMBER: US/09/347,343A

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;  CURRENT FILING DATE: 1999-07-02
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 32
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: synthetic oligonucleotide
US-09-347-343-32

  Query Match            100.0%;  Score 22;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.075;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 3
US-09-820-484-1
; Sequence 1, Application US/09820484
; Patent No. 6534062
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Cho, Hearn Jay
;  APPLICANT:  Richman, Douglas
;  APPLICANT:  Horner, Anthony A.
;  TITLE OF INVENTION: Method for Increasing a Cytotoxic T
;  TITLE OF INVENTION:  Lymphocyte Response in vivo.
;  FILE REFERENCE: 06510-188US1
;  CURRENT APPLICATION NUMBER: US/09/820,484
;  CURRENT FILING DATE:  2001-03-28
;  PRIOR APPLICATION NUMBER: US 60/192,537
;  PRIOR FILING DATE: 2000-03-28
;  PRIOR APPLICATION NUMBER: US 60/203,567
;  PRIOR FILING DATE: 2000-05-11
;  PRIOR APPLICATION NUMBER: US 60/215,895
;  PRIOR FILING DATE: 2000-07-05
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Disulfide-linked phosphorothioate ISS-ODN
;   NAME/KEY: modified_base
;   LOCATION: (1)...(1)
;   OTHER INFORMATION: disulfide thymine
US-09-820-484-1

  Query Match            100.0%;  Score 22;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.075;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 4
US-09-820-484-3
; Sequence 3, Application US/09820484
; Patent No. 6534062
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Cho, Hearn Jay
;  APPLICANT:  Richman, Douglas
;  APPLICANT:  Horner, Anthony A.
;  TITLE OF INVENTION: Method for Increasing a Cytotoxic T
;  TITLE OF INVENTION:  Lymphocyte Response in vivo.
;  FILE REFERENCE: 06510-188US1
;  CURRENT APPLICATION NUMBER: US/09/820,484
;  CURRENT FILING DATE:  2001-03-28
;  PRIOR APPLICATION NUMBER: US 60/192,537
;  PRIOR FILING DATE: 2000-03-28
;  PRIOR APPLICATION NUMBER: US 60/203,567
;  PRIOR FILING DATE: 2000-05-11
;  PRIOR APPLICATION NUMBER: US 60/215,895
;  PRIOR FILING DATE: 2000-07-05
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: phosphorothioate ISS-ODN
US-09-820-484-3

  Query Match            100.0%;  Score 22;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.075;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 5
US-09-774-403A-1
; Sequence 1, Application US/09774403A
; Patent No. 6552006
; GENERAL INFORMATION:
;  APPLICANT: Eyal Raz
;  APPLICANT:  Richard Kornbluth
;  APPLICANT:  Antonio Catanzaro
;  APPLICANT:  Tomoko Hayashi
;  APPLICANT:  Dennis Carson
;  TITLE OF INVENTION: Immunomodulatory Polynucleotides in
;  TITLE OF INVENTION:  Treatment of Infection by an Intracellular Pathogen
;  FILE REFERENCE: UCAL166
;  CURRENT APPLICATION NUMBER: US/09/774,403A
;  CURRENT FILING DATE:  2002-04-15
;  PRIOR APPLICATION NUMBER: 60/179,353
;  PRIOR FILING DATE: 2000-01-31
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Immunomodulatory sequence
US-09-774-403A-1

  Query Match            100.0%;  Score 22;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.075;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 6
US-09-296-477-2
; Sequence 2, Application US/09296477A
; Patent No. 6589940
; GENERAL INFORMATION:
;  APPLICANT: RAZ, E.
;  APPLICANT: SCHWARTZ, D.
;  APPLICANT: ROMAN, M.
;  APPLICANT: DINA, D.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,
;  TITLE OF INVENTION: COMPOSITIONS THEREOF AND METHODS OF USE
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;  TITLE OF INVENTION: THEREOF
;  FILE REFERENCE: 377882000420
;  CURRENT APPLICATION NUMBER: US/09/296,477A
;  CURRENT FILING DATE: 1999-04-22
;  EARLIER APPLICATION NUMBER: 09/092,329
;  EARLIER FILING DATE: 1998-06-05
;  EARLIER APPLICATION NUMBER: 60/048,793
;  EARLIER FILING DATE: 1997-06-06
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-09-296-477-2

  Query Match             100.0%;  Score 22;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.075;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 7
US-09-308-036A-1
; Sequence 1, Application US/09308036A
; Patent No. 6610661
; GENERAL INFORMATION:
;  APPLICANT: Carson, Dennis A.
;  APPLICANT:  Raz, Eyal
;  APPLICANT:  Roman, Mark
;  TITLE OF INVENTION: Immunostimulatory
;  TITLE OF INVENTION:  Polynucleotide/Immunomodulatory Molecule Conjugates
;  FILE REFERENCE: 6510-172CIP
;  CURRENT APPLICATION NUMBER: US/09/308,036A
;  CURRENT FILING DATE:  2000-02-16
;  PRIOR APPLICATION NUMBER: PCT/US97/19004
;  PRIOR FILING DATE: 1997-10-09
;  PRIOR APPLICATION NUMBER: 60/028,118
;  PRIOR FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: DY1018 polynucleotide
US-09-308-036A-1

  Query Match             100.0%;  Score 22;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.075;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 8
US-09-791-500-1
; Sequence 1, Application US/09791500
; Patent No. 6613751
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Rachmilewitz, Daniel
;  TITLE OF INVENTION: Method for Treating Inflammatory Bowel
;  TITLE OF INVENTION:  Disease and Other Forms of Gastrointestinal Inflammation.
;  FILE REFERENCE: 6510-202US1
;  CURRENT APPLICATION NUMBER: US/09/791,500
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic polynucleotide sequence
US-09-791-500-1

  Query Match             100.0%;  Score 22;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.075;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 9
US-09-565-906-2
; Sequence 2, Application US/09565906
; Patent No. 6737066
; GENERAL INFORMATION:
;  APPLICANT:  Moss, Ronald B.
;  TITLE OF INVENTION:  HIV Immunogenic Compositions and Methods
;  FILE REFERENCE:  P-IM 4029
;  CURRENT APPLICATION NUMBER: US/09/565,906
;  CURRENT FILING DATE:  2000-05-05
;  PRIOR APPLICATION NUMBER:  US 60/132,762
;  PRIOR FILING DATE:  1999-05-06
;  PRIOR APPLICATION NUMBER:  US 60/150,667
;  PRIOR FILING DATE:  1999-08-25
;  NUMBER OF SEQ ID NOS:  4
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: phosphorothioate-modified synthetic
;   OTHER INFORMATION: oligodeoxynucleotide
US-09-565-906-2

  Query Match             100.0%;  Score 22;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.075;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 10
US-09-296-477-15
; Sequence 15, Application US/09296477A
; Patent No. 6589940
; GENERAL INFORMATION:
;  APPLICANT: RAZ, E.
;  APPLICANT: SCHWARTZ, D.
;  APPLICANT: ROMAN, M.
;  APPLICANT: DINA, D.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,
;  TITLE OF INVENTION: COMPOSITIONS THEREOF AND METHODS OF USE
;  TITLE OF INVENTION: THEREOF
;  FILE REFERENCE: 377882000420
;  CURRENT APPLICATION NUMBER: US/09/296,477A
;  CURRENT FILING DATE: 1999-04-22
;  EARLIER APPLICATION NUMBER: 09/092,329
;  EARLIER FILING DATE: 1998-06-05
;  EARLIER APPLICATION NUMBER: 60/048,793
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; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (11)...(11)
; OTHER INFORMATION: 5-bromocytosine
US-09-296-477-15

Query Match 95.5%; Score 21; DB 4; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.24;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||| ||||||||||
Db 1 TGACTGTGAANGTTCGAGATGA 22

RESULT 11
US-09-092-314-2
; Sequence 2, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-2

Query Match 92.7%; Score 20.4; DB 3; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.49;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
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Db 1 TGACTGTGAACGTTAGAGATGA 22

RESULT 12
US-09-820-484-2
; Sequence 2, Application US/09820484
; Patent No. 6534062
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Cho, Hearn Jay
; APPLICANT: Richman, Douglas
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Method for Increasing a Cytotoxic T
; TITLE OF INVENTION: Lymphocyte Response in vivo.
; FILE REFERENCE: 06510-188US1
; CURRENT APPLICATION NUMBER: US/09/820,484
; CURRENT FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/192,537
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/203,567
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/215,895
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutated ODN
; NAME/KEY: modified_base
; LOCATION: (1)...(1)
; OTHER INFORMATION: disulfide thymine
US-09-820-484-2

Query Match 92.7%; Score 20.4; DB 4; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.49;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||| ||||||||||
Db 1 TGACTGTGAACCTTCGAGATGA 22

RESULT 13
US-09-820-484-6
; Sequence 6, Application US/09820484
; Patent No. 6534062
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Cho, Hearn Jay
; APPLICANT: Richman, Douglas
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Method for Increasing a Cytotoxic T
; TITLE OF INVENTION: Lymphocyte Response in vivo.
; FILE REFERENCE: 06510-188US1
; CURRENT APPLICATION NUMBER: US/09/820,484
; CURRENT FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/192,537
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/203,567
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/215,895
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutated control ODN
US-09-820-484-6

Query Match 92.7%; Score 20.4; DB 4; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.49;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||| ||||||||||
Db 1 TGACTGTGAACCTTCGAGATGA 22

RESULT 14
US-09-774-403A-2
; Sequence 2, Application US/09774403A
; Patent No. 6552006
; GENERAL INFORMATION:
; APPLICANT: Eyal Raz
; APPLICANT: Richard Kornbluth

; APPLICANT: Antonio Catanzaro
; APPLICANT: Tomoko Hayashi
; APPLICANT: Dennis Carson
; TITLE OF INVENTION: Immunomodulatory Polynucleotides in
; TITLE OF INVENTION: Treatment of Infection by an Intracellular Pathogen
; FILE REFERENCE: UCAL166
; CURRENT APPLICATION NUMBER: US/09/774,403A
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: 60/179,353
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Control sequence
US-09-774-403A-2

Query Match 92.7%; Score 20.4; DB 4; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.49;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||.|||||||||||
Db 1 TGACTGTGAAGGTTCGAGATGA 22

RESULT 15
US-09-296-477-1
; Sequence 1, Application US/09296477A
; Patent No. 6589940
; GENERAL INFORMATION:
; APPLICANT: RAZ, E.
; APPLICANT: SCHWARTZ, D.
; APPLICANT: ROMAN, M.
; APPLICANT: DINA, D.
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,
; TITLE OF INVENTION: COMPOSITIONS THEREOF AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 377882000420
; CURRENT APPLICATION NUMBER: US/09/296,477A
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: 09/092,329
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/048,793
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-296-477-1

Query Match 92.7%; Score 20.4; DB 4; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.49;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
|||| ||||||||||||||||
Db 1 TGACCGTGAACGTTCGAGATGA 22

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Job time : 95 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 28, 2005, 22:47:02 ; Search time 319 Seconds
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Title: US-09-802-376-1
Perfect score: 22
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5552208 seqs, 2979665951 residues

Total number of hits satisfying chosen parameters: 11104416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	22	100.0	22	9	US-09-802-685-1	Sequence 1, Appli
3	22	100.0	22	9	US-09-791-500-1	Sequence 1, Appli
4	22	100.0	22	9	US-09-802-376-1	Sequence 1, Appli
5	22	100.0	22	9	US-09-774-403A-1	Sequence 1, Appli
6	22	100.0	22	9	US-09-802-370-1	Sequence 1, Appli
7	22	100.0	22	9	US-09-802-445-1	Sequence 1, Appli
8	22	100.0	22	9	US-09-820-484-1	Sequence 1, Appli
9	22	100.0	22	9	US-09-820-484-3	Sequence 3, Appli
10	22	100.0	22	9	US-09-828-505-1	Sequence 1, Appli
11	22	100.0	22	9	US-09-967-881-2	Sequence 2, Appli
12	22	100.0	22	10	US-09-927-422A-1	Sequence 1, Appli
13	22	100.0	22	10	US-09-738-046A-3	Sequence 3, Appli
14	22	100.0	22	10	US-09-927-884-1	Sequence 1, Appli
15	22	100.0	22	10	US-09-802-359-1	Sequence 1, Appli
16	22	100.0	22	10	US-09-967-464-19	Sequence 19, Appl
17	22	100.0	22	10	US-09-848-986-1	Sequence 1, Appli
18	22	100.0	22	14	US-10-056-420-4	Sequence 4, Appli
19	22	100.0	22	14	US-10-033-243-2	Sequence 2, Appli
20	22	100.0	22	14	US-10-033-243-40	Sequence 40, Appl
21	22	100.0	22	14	US-10-033-243-59	Sequence 59, Appl
22	22	100.0	22	14	US-10-214-288-1	Sequence 1, Appli
23	22	100.0	22	14	US-10-099-512-1	Sequence 1, Appli
24	22	100.0	22	14	US-10-229-208-19	Sequence 19, Appl
25	22	100.0	22	15	US-10-253-117-32	Sequence 32, Appl
26	22	100.0	22	15	US-10-233-121A-1	Sequence 1, Appli
27	22	100.0	22	15	US-10-219-143-1	Sequence 1, Appli
28	22	100.0	22	15	US-10-214-799-2	Sequence 2, Appli
29	22	100.0	22	15	US-10-340-275-1	Sequence 1, Appli
30	22	100.0	22	15	US-10-340-275-3	Sequence 3, Appli
31	22	100.0	22	15	US-10-339-885-1	Sequence 1, Appli
32	22	100.0	22	15	US-10-339-885-3	Sequence 3, Appli
33	22	100.0	22	16	US-10-176-883-2	Sequence 2, Appli
34	22	100.0	22	16	US-10-176-883-24	Sequence 24, Appl
35	22	100.0	22	16	US-10-176-883-79	Sequence 79, Appl
36	22	100.0	22	16	US-10-176-883-134	Sequence 134, App
37	22	100.0	22	16	US-10-412-151-1	Sequence 1, Appli
38	22	100.0	22	16	US-10-177-826-2	Sequence 2, Appli
39	22	100.0	22	16	US-10-177-826-24	Sequence 24, Appl
40	22	100.0	22	16	US-10-177-826-79	Sequence 79, Appl
41	22	100.0	22	16	US-10-177-826-134	Sequence 134, App
42	22	100.0	22	17	US-10-353-917-1	Sequence 1, Appli
43	22	100.0	22	17	US-10-357-760-1	Sequence 1, Appli
44	22	100.0	22	17	US-10-328-578-2	Sequence 2, Appli
45	22	100.0	22	17	US-10-328-578-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-09-802-686-1
; Sequence 1, Application US/09802686
; Patent No. US20010046967A1
; GENERAL INFORMATION:
; APPLICANT: Dynavax Technologies Corporation
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF PREVENTING AND TREATING
; TITLE OF INVENTION: RESPIRATORY VIRAL INFECTION USING IMMUNOMODULATORY
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCES
; FILE REFERENCE: 377882000900
; CURRENT APPLICATION NUMBER: US/09/802,686
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,583
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-686-1

Query Match 100.0%; Score 22; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATGA 22
||||||||||||||||||||||
Db 1 TGACTGTGAACGTTCGAGATGA 22

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RESULT 2
US-09-802-685-1
; Sequence 1, Application US/09802685
; Patent No. US20020028784A1
; GENERAL INFORMATION:
;  APPLICANT: Van Nest, Gary
;  APPLICANT:  Eiden, Joseph J., Jr.
;  TITLE OF INVENTION: METHODS OF PREVENTING AND TREATING VIRAL
;  TITLE OF INVENTION:  INFECTIONS USING IMMUNOMODULATORY POLYNUCLEOTIDE SEQUENCES
;  FILE REFERENCE: 377882001600
;  CURRENT APPLICATION NUMBER: US/09/802,685
;  CURRENT FILING DATE:  2001-03-09
;  PRIOR APPLICATION NUMBER: U.S. 60/188,302
;  PRIOR FILING DATE: 2000-03-10
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-09-802-685-1

  Query Match             100.0%;  Score 22;  DB 9;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.4;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 3
US-09-791-500-1
; Sequence 1, Application US/09791500
; Patent No. US20020042387A1
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Rachmilewitz, Daniel
;  TITLE OF INVENTION: Method for Treating Inflammatory Bowel
;  TITLE OF INVENTION:  Disease and Other Forms of Gastrointestinal Inflammation.
;  FILE REFERENCE: 6510-202US1
;  CURRENT APPLICATION NUMBER: US/09/791,500
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic polynucleotide sequence
US-09-791-500-1

  Query Match             100.0%;  Score 22;  DB 9;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.4;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 4
US-09-802-376-1
; Sequence 1, Application US/09802376
; Patent No. US20020055477A1
; GENERAL INFORMATION:
;  APPLICANT: Van Nest, Gary
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
;  FILE REFERENCE: 37788201700
;  CURRENT APPLICATION NUMBER: US/09/802,376
;  CURRENT FILING DATE:  2001-03-09
;  PRIOR APPLICATION NUMBER: 60/188,557
;  PRIOR FILING DATE: 2000-03-10
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-09-802-376-1

  Query Match             100.0%;  Score 22;  DB 9;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.4;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 5
US-09-774-403A-1
; Sequence 1, Application US/09774403A
; Publication No. US20020086295A1
; GENERAL INFORMATION:
;  APPLICANT: Eyal Raz
;  APPLICANT:  Richard Kornbluth
;  APPLICANT:  Antonio Catanzaro
;  APPLICANT:  Tomoko Hayashi
;  APPLICANT:  Dennis Carson
;  TITLE OF INVENTION: Immunomodulatory Polynucleotides in
;  TITLE OF INVENTION:  Treatment of Infection by an Intracellular Pathogen
;  FILE REFERENCE: UCAL166
;  CURRENT APPLICATION NUMBER: US/09/774,403A
;  CURRENT FILING DATE:  2002-04-15
;  PRIOR APPLICATION NUMBER: 60/179,353
;  PRIOR FILING DATE: 2000-01-31
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Immunomodulatory sequence
US-09-774-403A-1

  Query Match             100.0%;  Score 22;  DB 9;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.4;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 6
US-09-802-370-1
; Sequence 1, Application US/09802370
; Patent No. US20020098199A1
; GENERAL INFORMATION:
;  APPLICANT: Van Nest, Gary
;  APPLICANT:  Eiden, Joseph J. Jr.
;  TITLE OF INVENTION: METHODS OF SUPPRESSING HEPATITIS VIRUS
;  TITLE OF INVENTION:  INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE SEQUENCES
;  FILE REFERENCE: 377882001200
;  CURRENT APPLICATION NUMBER: US/09/802,370
;  CURRENT FILING DATE:  2001-09-24
;  PRIOR APPLICATION NUMBER: 60/188,301
;  PRIOR FILING DATE: 2000-03-10
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;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-09-802-370-1

  Query Match             100.0%;  Score 22;  DB 9;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.4;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 7
US-09-802-445-1
; Sequence 1, Application US/09802445
; Patent No. US20020107212A1
; GENERAL INFORMATION:
;  APPLICANT: Van Nest, Gary
;  APPLICANT:  Eiden, Joseph J. Jr.
;  TITLE OF INVENTION: METHODS OF REDUCING PAPILLOMAVIRUS INFECTION USING IMMUNOMODULATC
;  TITLE OF INVENTION:  POLYNUCLEOTIDE SEQUENCES
;  FILE REFERENCE: 377882001300
;  CURRENT APPLICATION NUMBER: US/09/802,445
;  CURRENT FILING DATE:  2001-09-24
;  PRIOR APPLICATION NUMBER: 60/188,265
;  PRIOR FILING DATE: 2000-03-10
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-09-802-445-1

  Query Match             100.0%;  Score 22;  DB 9;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.4;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 8
US-09-820-484-1
; Sequence 1, Application US/09820484
; Patent No. US20020142977A1
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Cho, Hearn Jay
;  APPLICANT:  Richman, Douglas
;  APPLICANT:  Horner, Anthony A.
;  TITLE OF INVENTION: Method for Increasing a Cytotoxic T
;  TITLE OF INVENTION:  Lymphocyte Response in vivo.
;  FILE REFERENCE: 06510-188US1
;  CURRENT APPLICATION NUMBER: US/09/820,484
;  CURRENT FILING DATE:  2001-03-28
;  PRIOR APPLICATION NUMBER: US 60/192,537
;  PRIOR FILING DATE: 2000-03-28
;  PRIOR APPLICATION NUMBER: US 60/203,567
;  PRIOR FILING DATE: 2000-05-11
;  PRIOR APPLICATION NUMBER: US 60/215,895
;  PRIOR FILING DATE: 2000-07-05
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Disulfide-linked phosphorothioate ISS-ODN
;   NAME/KEY: modified_base
;   LOCATION: (1)...(1)
;   OTHER INFORMATION: disulfide thymine
US-09-820-484-1

  Query Match             100.0%;  Score 22;  DB 9;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.4;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 9
US-09-820-484-3
; Sequence 3, Application US/09820484
; Patent No. US20020142977A1
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Cho, Hearn Jay
;  APPLICANT:  Richman, Douglas
;  APPLICANT:  Horner, Anthony A.
;  TITLE OF INVENTION: Method for Increasing a Cytotoxic T
;  TITLE OF INVENTION:  Lymphocyte Response in vivo.
;  FILE REFERENCE: 06510-188US1
;  CURRENT APPLICATION NUMBER: US/09/820,484
;  CURRENT FILING DATE:  2001-03-28
;  PRIOR APPLICATION NUMBER: US 60/192,537
;  PRIOR FILING DATE: 2000-03-28
;  PRIOR APPLICATION NUMBER: US 60/203,567
;  PRIOR FILING DATE: 2000-05-11
;  PRIOR APPLICATION NUMBER: US 60/215,895
;  PRIOR FILING DATE: 2000-07-05
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: phosphorothioate ISS-ODN
US-09-820-484-3

  Query Match             100.0%;  Score 22;  DB 9;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.4;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 10
US-09-828-505-1
; Sequence 1, Application US/09828505
; Patent No. US20020142978A1
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Takabayashi, Kenji
;  APPLICANT:  Nguyen, Minh-Duc
;  TITLE OF INVENTION: Synergistic Improvements to
;  TITLE OF INVENTION:  Polynucleotide Vaccines
;  FILE REFERENCE: 6510-203
;  CURRENT APPLICATION NUMBER: US/09/828,505
;  CURRENT FILING DATE:  2001-04-06
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;  PRIOR APPLICATION NUMBER: 60/195,890
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Immunomodulatory nucleic acid sequence
US-09-828-505-1

  Query Match             100.0%;  Score 22;  DB 9;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.4;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 11
US-09-967-881-2
; Sequence 2, Application US/09967881
; Publication No. US20020192184A1
; GENERAL INFORMATION:
;  APPLICANT: Assistance Publique - Hopitaux de Paris
;  APPLICANT:  Institut National de la Sante et de la Recherche M
;  APPLICANT:  Carpentier, Antoine
;  TITLE OF INVENTION: Use of Stabilised Oligonucleotides for Preparing A Medicament wit
;  TITLE OF INVENTION:  Antitumor Activity
;  FILE REFERENCE: 267/246 US
;  CURRENT APPLICATION NUMBER: US/09/967,881
;  CURRENT FILING DATE:  2001-09-28
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Oligodeoxynucleotide
US-09-967-881-2

  Query Match             100.0%;  Score 22;  DB 9;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.4;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 12
US-09-927-422A-1
; Sequence 1, Application US/09927422A
; Publication No. US20030022852A1
; GENERAL INFORMATION:
;  APPLICANT: Van Nest, Gary
;  APPLICANT:  Tuck, Stephen
;  APPLICANT:  Fearon, Karen L.
;  APPLICANT:  Dina, Dino
;  TITLE OF INVENTION: BIODEGRADABLE IMMUNOMODULATORY
;  TITLE OF INVENTION:  FORMULATIONS AND METHODS FOR USE THEREOF
;  FILE REFERENCE: 377882001420
;  CURRENT APPLICATION NUMBER: US/09/927,422A
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: U.S. 09/802,359
;  PRIOR FILING DATE: 2001-03-09
;  PRIOR APPLICATION NUMBER: U.S. 60/188,30
;  PRIOR FILING DATE: 2000-03-10
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-09-927-422A-1

  Query Match             100.0%;  Score 22;  DB 10;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.4;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 13
US-09-738-046A-3
; Sequence 3, Application US/09738046A
; Publication No. US20030054007A1
; GENERAL INFORMATION:
;  APPLICANT: FELGNER, PHILIP L.
;  APPLICANT:  ZELPHATI, OLIVIER
;  TITLE OF INVENTION: INTRACELLULAR PROTEIN DELIVERY
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS OF USE
;  FILE REFERENCE: GTSYS.004A
;  CURRENT APPLICATION NUMBER: US/09/738,046A
;  CURRENT FILING DATE:  2000-12-15
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: artificial sequence containing CpG sequence
US-09-738-046A-3

  Query Match             100.0%;  Score 22;  DB 10;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.4;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 14
US-09-927-884-1
; Sequence 1, Application US/09927884
; Publication No. US20030059773A1
; GENERAL INFORMATION:
;  APPLICANT: Van Nest, Gary
;  APPLICANT:  Tuck, Stephen
;  APPLICANT:  Fearon, Karen L.
;  APPLICANT:  Dina, Dino
;  TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND
;  TITLE OF INVENTION:  METHODS FOR USE THEREOF
;  FILE REFERENCE: 377882001720
;  CURRENT APPLICATION NUMBER: US/09/927,884
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: U.S. 09/802,376
;  PRIOR FILING DATE: 2001-03-09
;  PRIOR APPLICATION NUMBER: U.S. 60/188,557
;  PRIOR FILING DATE: 2000-03-10
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
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```
;   OTHER INFORMATION: Polynucleotide containing CG
US-09-927-884-1

  Query Match             100.0%;  Score 22;  DB 10;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.4;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 15
US-09-802-359-1
; Sequence 1, Application US/09802359
; Publication No. US20030129251A1
; GENERAL INFORMATION:
;  APPLICANT: Van Nest, Gary
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
;  FILE REFERENCE: 37788201400
;  CURRENT APPLICATION NUMBER: US/09/802,359
;  CURRENT FILING DATE:  2001-03-09
;  PRIOR APPLICATION NUMBER: 60/188,303
;  PRIOR FILING DATE: 2000-03-10
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-09-802-359-1

  Query Match             100.0%;  Score 22;  DB 10;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.4;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


Search completed: March 28, 2005, 23:57:24
Job time : 321 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 28, 2005, 22:36:17 ; Search time 1991 Seconds
(without alignments)
420.600 Million cell updates/sec

Title: US-09-802-376-1
Perfect score: 22
Sequence: 1 tgactgtgaacgttcgagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	18.8	85.5	521	8	BH859011	BH859011 S5_182b_t
2	18.4	83.6	571	4	BM042508	BM042508 603615795
c 3	17.8	80.9	492	9	CE751403	CE751403 tigr-gss-
c 4	17.8	80.9	561	8	AZ755668	AZ755668 ev02g09.x
5	17.8	80.9	867	8	BZ558601	BZ558601 pa98401_2
6	17.8	80.9	961	4	BF971856	BF971856 602240444
c 7	17.4	79.1	489	8	AZ060178	AZ060178 RPCI-23-4
c 8	17.4	79.1	530	8	AZ886419	AZ886419 RPCI-23-1
9	17.2	78.2	374	8	AQ245026	AQ245026 HS_2056_B
10	17.2	78.2	408	8	AZ536502	AZ536502 110300_96
11	17.2	78.2	424	2	BE723539	BE723539 193384_MA
c 12	17.2	78.2	427	7	CO514528	CO514528 s13dSG43G
13	17.2	78.2	463	1	AU083559	AU083559 AU083559
14	17.2	78.2	479	1	AU089685	AU089685 AU089685
15	17.2	78.2	513	4	BJ094274	BJ094274 BJ094274
16	17.2	78.2	515	7	CF447937	CF447937 EST684282
17	17.2	78.2	519	4	BI796581	BI796581 H049F08 E
18	17.2	78.2	571	4	BM037907	BM037907 S114c07 S
19	17.2	78.2	595	9	CC952473	CC952473 BOICU52TR
c 20	17.2	78.2	617	6	CD488495	CD488495 T10_D04 T
21	17.2	78.2	619	9	CL956886	CL956886 OsIRUA005
22	17.2	78.2	633	4	BJ808940	BJ808940 BJ808940
c 23	17.2	78.2	634	7	CR286398	CR286398 CR286398
c 24	17.2	78.2	655	6	CD487922	CD487922 T02_B03 T
25	17.2	78.2	726	5	BW071434	BW071434 BW071434
c 26	17.2	78.2	767	6	CB685128	CB685128 OSJNEf15E
c 27	17.2	78.2	812	6	CB644373	CB644373 OSJNEb05I
28	17.2	78.2	844	6	CB685127	CB685127 OSJNEf15E
c 29	17.2	78.2	852	9	CL670249	CL670249 PRI0161c_
30	17.2	78.2	882	7	CF378583	CF378583 AGENCOURT
c 31	17.2	78.2	972	9	CNS05PD9	AL347814 Tetraodon
32	17.2	78.2	1028	6	CA139194	CA139194 SCEQRT209
33	17.2	78.2	1852	9	CL487297	CL487297 SAIL_44_G
c 34	17.2	78.2	2481	3	AK037625	AK037625 Mus muscu
35	16.8	76.4	105	1	AA094019	AA094019 cl1619.se
c 36	16.8	76.4	496	9	CB537167	CB537167 tigr-gss-
37	16.8	76.4	523	8	AZ483488	AZ483488 1M0309M12
38	16.8	76.4	526	8	AZ501799	AZ501799 1M0340J17
c 39	16.8	76.4	628	6	CA380211	CA380211 659460 NC
40	16.8	76.4	645	6	CB576172	CB576172 AMGNNUC:C
c 41	16.8	76.4	654	7	CO079691	CO079691 GR__Ea42K
c 42	16.8	76.4	678	6	CA373611	CA373611 647793 NC
c 43	16.8	76.4	681	1	AV732648	AV732648 AV732648
44	16.8	76.4	683	7	CV510488	CV510488 kc59h08.y
45	16.8	76.4	705	2	AW916461	AW916461 EST347765

ALIGNMENTS

RESULT 1
BH859011
LOCUS BH859011 521 bp DNA linear GSS 13-NOV-2002
DEFINITION S5_182b_t7 Mouse Retroviral Tagged Cancer Gene Database Mus musculus genomic clone S5_182b, genomic survey sequence.
ACCESSION BH859011
VERSION BH859011.1 GI:21709832
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 521)
AUTHORS Suzuki,T., Shen,H., Akagi,K., Morse,H.C., Malley,J.D., Naiman,D.Q., Jenkins,N.A. and Copeland,N.G.
TITLE New genes involved in cancer identified by retroviral tagging
JOURNAL Nat. Genet. 32 (1), 166-174 (2002)
MEDLINE 22194816
PUBMED 12185365
COMMENT Contact: Copeland NG
Mouse Cancer Genetics Program
National Cancer Institute
Bldg. 539, Rm. 229, Frederick, MD 21702-1201, USA
Tel: 301 846 1260
Fax: 301 846 6666
Email: copeland@ncifcrf.gov
Class: PCR with specific primers.
FEATURES Location/Qualifiers
source 1. .521
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="S5_182b"
/sex="female"
/tissue_type="leukemia"
/clone_lib="Mouse Retroviral Tagged Cancer Gene Database"
/note="Inverse PCR method
(http://genome2.ncifcrf.gov/RTCGD)"
ORIGIN

Query Match 85.5%; Score 18.8; DB 8; Length 521;
Best Local Similarity 90.9%; Pred. No. 91;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 TGACTGTGAACGTTCGAGATGA 22
              |||||||||| | ||||||||
Db        116 TGACTGTGAACATGCGAGATGA 137
```

```
RESULT 2
BM042508
LOCUS       BM042508                571 bp    mRNA    linear   EST 07-NOV-2001
DEFINITION  603615795T1 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:5420734 3',
            mRNA sequence.
ACCESSION   BM042508
VERSION     BM042508.1  GI:16771788
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 571)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1875  row: m  column: 23
            High quality sequence start: 44
            High quality sequence stop: 411.
FEATURES             Location/Qualifiers
     source          1. .571
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5420734"
                     /tissue_type="melanotic melanoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_112"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             83.6%;  Score 18.4;  DB 4;  Length 571;
  Best Local Similarity   95.0%;  Pred. No. 1.5e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGAT 20
              |||||||||||||||| ||||
Db        504 TGACTGTGAACGTTCTAGAT 523


RESULT 3
CE751403/c
LOCUS       CE751403                492 bp    DNA     linear   GSS 30-SEP-2003
DEFINITION  tigr-gss-dog-17000369615400 Dog Library Canis familiaris genomic,
            genomic survey sequence.
ACCESSION   CE751403
VERSION     CE751403.1  GI:37092020
KEYWORDS    GSS.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 492)
  AUTHORS   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
            Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
            Venter,J.C.
  TITLE     The dog genome: survey sequencing and comparative analysis
  JOURNAL   Science 301 (5641), 1898-1903 (2003)
  MEDLINE   22875432
   PUBMED   14512627
COMMENT     Contact: Kirkness EF
            The Institute for Genomic Research
            Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
            Rockville, MD 20850, USA
            Tel: 301-838-0200
            Fax: 301-838-0208
            Email: ekirknes@tigr.org
            Class: shotgun.
FEATURES             Location/Qualifiers
     source          1. .492
                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /strain="Standard Poodle"
                     /db_xref="taxon:9615"
                     /clone_lib="Dog Library"
                     /note="Site_1: BstXI; Libraries were prepared from
                     peripheral blood"
ORIGIN

  Query Match             80.9%;  Score 17.8;  DB 9;  Length 492;
  Best Local Similarity   90.5%;  Pred. No. 3e+02;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATG 21
              |||||||||||||| || ||||
Db         36 TGACTGTGAACGTGCGGGATG 16


RESULT 4
AZ755668/c
LOCUS       AZ755668                561 bp    DNA     linear   GSS 01-MAR-2001
DEFINITION  ev02g09.x1 PAX3 CASTing Library 'ev' Homo sapiens genomic clone
            ev02g09 random, genomic survey sequence.
ACCESSION   AZ755668
VERSION     AZ755668.1  GI:13175090
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 561)
  AUTHORS   Barber,T.D., Barber,M.C., Tomescu,O., Barr,F.G., Ruben,S. and
            Friedman,T.B.
  TITLE     Identification of Target Genes Regulated by PAX3 and PAX3--FKHR in
            Embryogenesis and Alveolar Rhabdomyosarcoma
  JOURNAL   Genomics 79 (3), 278-284 (2002)
  MEDLINE   21853298
   PUBMED   11863357
COMMENT     Contact: Friedman TB
            Laboratory of Molecular Genetics
            National Institute on Deafness and Other Communication Disorders,
            National Institutes of Health
            5 Research Court, Room 2A-15, Rockville, MD 20850, USA
            Tel: 301 402 7580
            Fax: 301 496 7882
            Email: friedman@nidcd.nih.gov
            Plate: 02  row: g  column: 09
            Seq primer: -21M13 forward primer (ABI)
            Class: random plasmid subclone.
FEATURES             Location/Qualifiers
     source          1. .561
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="ev02g09"
                     /sex="Male"
                     /lab_host="DH10B"
                     /clone_lib="PAX3 CASTing Library 'ev'"
```

/note="Vector: pGEM-T Easy; Human genomic DNA was partially digested with Sau3AI, ligated to ds linkers, and enriched for binding to human PAX3dQ+ protein using a Whole Genome PCR-based strategy. DNA fragments containing putative PAX3dQ+ binding sites were amplified by PCR and cloned into pGEM-T Easy (Promega). The ligation products were transformed into DH10B electrocompetent cells (Life Technologies)."

ORIGIN

Query Match 80.9%; Score 17.8; DB 8; Length 561;
Best Local Similarity 90.5%; Pred. No. 3.1e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTCGAGATG 21
||||||||||||| ||||||
Db 461 TGACTGTGAACGTCAGAGATG 441

RESULT 5
BZ558601
LOCUS BZ558601 867 bp DNA linear GSS 17-DEC-2002
DEFINITION pa98401_292.s1 pacs2-164 Pseudomonas aeruginosa genomic clone pa98401_292, genomic survey sequence.
ACCESSION BZ558601
VERSION BZ558601.1 GI:27173329
KEYWORDS GSS.
SOURCE Pseudomonas aeruginosa
ORGANISM Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.
REFERENCE 1 (bases 1 to 867)
AUTHORS Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M., Burns,J.L., Kaul,R. and Olsen,M.V.
TITLE Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
JOURNAL J. Bacteriol. (2002) In press
COMMENT Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.
FEATURES Location/Qualifiers
source 1. .867
/organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="2-164"
/db_xref="taxon:287"
/clone="pa98401_292"
/clone_lib="pacs2-164"
/note="clinical isolate 2-164 Whole genomic shotgun library."

ORIGIN

Query Match 80.9%; Score 17.8; DB 8; Length 867;
Best Local Similarity 90.5%; Pred. No. 3.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GACTGTGAACGTTCGAGATGA 22
|||||||||| ||||| ||||
Db 724 GACTGTGAACCTTCGATATGA 744

RESULT 6
BF971856
LOCUS BF971856 961 bp mRNA linear EST 22-JAN-2001
DEFINITION 602240444F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4328890 5', mRNA sequence.
ACCESSION BF971856
VERSION BF971856.1 GI:12339071
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 961)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1189 row: h column: 11
High quality sequence stop: 555.
FEATURES Location/Qualifiers
source 1. .961
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4328890"
/tissue_type="leiomyosarcoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_46"
/note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 80.9%; Score 17.8; DB 4; Length 961;
Best Local Similarity 90.5%; Pred. No. 3.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GACTGTGAACGTTCGAGATGA 22
|||||||||||||| |||||
Db 650 GACTGTGAACGTTCCGGATGA 670

RESULT 7
AZ060178/c
LOCUS AZ060178 489 bp DNA linear GSS 30-MAR-2000
DEFINITION RPCI-23-405E23.TJ RPCI-23 Mus musculus genomic clone RPCI-23-405E23, genomic survey sequence.
ACCESSION AZ060178
VERSION AZ060178.1 GI:7351427
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 489)
AUTHORS Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P. and Fraser,C.M.
TITLE Mouse BAC End Sequences from Library RPCI-23
JOURNAL Unpublished (1999)
COMMENT Other_GSSs: RPCI-23-405E23.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200

```
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-23. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
            or from Resea ch Genetics (info@resgen.com). BAC end page:
            http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 405  row: E  column: 23
            Seq primer: SP6
            Class: BAC ends.
FEATURES              Location/Qualifiers
     source           1. .489
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="RPCI-23-405E23"
                      /sex="Female"
                      /lab_host="DH10B"
                      /clone_lib="RPCI-23"
                      /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
                      EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
                      brain genomic DNA was isolated and  partially digested
                      with a combination of EcoRI and EcoRI Methylase.   Size
                      selected DNA was cloned into the pBACe3.6 vector at the
                      EcoRI  sites.  The ligation products were transformed into
                      DH10B  electrocompetent cells (BRL Life Technologies).   "
ORIGIN

  Query Match             79.1%;  Score 17.4;  DB 8;  Length 489;
  Best Local Similarity   94.7%;  Pred. No. 4.9e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGA 19
              ||||||||||| |||||||
Db        170 TGACTGTGAACATTCGAGA 152


RESULT 8
AZ886419/c
LOCUS       AZ886419                 530 bp    DNA     linear   GSS 05-MAR-2001
DEFINITION  RPCI-23-182I6.TJ RPCI-23 Mus musculus genomic clone RPCI-23-182I6,
            genomic survey sequence.
ACCESSION   AZ886419
VERSION     AZ886419.1  GI:13205364
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 530)
  AUTHORS   Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S.,
            Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de
            Jong,P. and Fraser,C.M.
  TITLE     Mouse BAC End Sequences from Library RPCI-23
  JOURNAL   Unpublished (1999)
COMMENT     Other_GSSs: RPCI-23-182I6.TV
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-23. For BAC
            library availability, please contact Pieter de Jong
            (pdejong@mail.cho.org). Clones may be purchased from BACPAC
            Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
            page: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 182  row: I  column: 6
            Seq primer: SP6
            Class: BAC ends.
FEATURES              Location/Qualifiers
     source           1. .530
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="RPCI-23-182I6"
                      /sex="Female"
                      /lab_host="DH10B"
                      /clone_lib="RPCI-23"
                      /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
                      EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
                      brain genomic DNA was isolated and  partially digested
                      with a combination of EcoRI and EcoRI Methylase.   Size
                      selected DNA was cloned into the pBACe3.6 vector at the
                      EcoRI  sites.  The ligation products were transformed into
                      DH10B  electrocompetent cells (BRL Life Technologies).   "
ORIGIN

  Query Match             79.1%;  Score 17.4;  DB 8;  Length 530;
  Best Local Similarity   94.7%;  Pred. No. 4.9e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGA 19
              ||||||||||| |||||||
Db        189 TGACTGTGAACATTCGAGA 171


RESULT 9
AQ245026
LOCUS       AQ245026                 374 bp    DNA     linear   GSS 03-OCT-1998
DEFINITION  HS_2056_B1_E03_MR CIT Approved Human Genomic Sperm Library D Homo
            sapiens genomic clone Plate=2056 Col=5 Row=J, genomic survey
            sequence.
ACCESSION   AQ245026
VERSION     AQ245026.1  GI:3691600
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 374)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
  MEDLINE   99380589
   PUBMED   10449764
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Sequence Tagged Connector
            Plate: 2056  row: J  column: 5
            Class: BAC ends
            High quality sequence stop: 374.
FEATURES              Location/Qualifiers
     source           1. .374
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
                      /clone="Plate=2056 Col=5 Row=J"
                      /sex="male"
                      /clone_lib="CIT Approved Human Genomic Sperm Library D"
                      /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
                      E-Coli DH10B"
ORIGIN
```

```
  Query Match             78.2%;  Score 17.2;  DB 8;  Length 374;
  Best Local Similarity   86.4%;  Pred. No. 5.9e+02;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              |||||||||||| | ||||| |
Db        207 TGACTGTGAACGATTGAGATCA 228


RESULT 10
AZ536502
LOCUS       AZ536502                408 bp    DNA     linear   GSS 03-NOV-2000
DEFINITION  110300_96 Planococcus lilacinus DNA Planococcus lilacinus genomic,
            genomic survey sequence.
ACCESSION   AZ536502
VERSION     AZ536502.1  GI:11093449
KEYWORDS    GSS.
SOURCE      Planococcus lilacinus (lilac mealybug)
  ORGANISM  Planococcus lilacinus
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
            Coccoidea; Pseudococcidae; Planococcus.
REFERENCE   1  (bases 1 to 408)
  AUTHORS   Mohan,K.N. and Chandra,H.S.
  TITLE     Mealybug shotgun sequencing
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Mohan KN
            Microbiology and Cell Biology
            Indian Institute of Science
            Sir C.V. Raman Avenue, Bangalore, Karnataka 560012, India
            Email: mohan@mcbl.iisc.ernet.in
            Class: shotgun.
FEATURES             Location/Qualifiers
     source          1. .408
                     /organism="Planococcus lilacinus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:40930"
                     /clone_lib="Planococcus lilacinus DNA"
ORIGIN

  Query Match             78.2%;  Score 17.2;  DB 8;  Length 408;
  Best Local Similarity   86.4%;  Pred. No. 6e+02;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              |||||||||||  ||| ||||
Db        251 TGACTGTGAACGAACGATATGA 272


RESULT 11
BE723539
LOCUS       BE723539                424 bp    mRNA    linear   EST 25-APR-2001
DEFINITION  193384 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   BE723539
VERSION     BE723539.1  GI:10124826
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE   1  (bases 1 to 424)
  AUTHORS   Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,
            Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
            Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F.,
            Quackenbush,J. and Keele,J.W.
  TITLE     Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
  JOURNAL   Genome Res. 11 (4), 626-630 (2001)
  MEDLINE   21180013
   PUBMED   11282978
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 92  row: E  column: 14
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .424
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="MARC 4BOV"
                     /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                     Library made from pooled tissue from day 20 and day 40
                     embryos."
ORIGIN

  Query Match             78.2%;  Score 17.2;  DB 2;  Length 424;
  Best Local Similarity   86.4%;  Pred. No. 6e+02;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||| | |||||||| |||||||
Db        268 TGAGTCTGAACGTTAGAGATGA 289


RESULT 12
CO514528/c
LOCUS       CO514528                427 bp    mRNA    linear   EST 15-JUL-2004
DEFINITION  s13dSG43G0800066_327716 Glandular trichomes Medicago sativa cDNA,
            mRNA sequence.
ACCESSION   CO514528
VERSION     CO514528.1  GI:50319402
KEYWORDS    EST.
SOURCE      Medicago sativa
  ORGANISM  Medicago sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1  (bases 1 to 427)
  AUTHORS   Aziz,N., May,G.D., Paiva,N.L. and Dixon,R.A.
  TITLE     Alfalfa trichome Expressed Sequence Tags from the Samuel Roberts
            Noble Foundation - Center for Medicago Genomics Research
  JOURNAL   Unpublished (2004)
COMMENT     Contact: May GD
            Plant Biology Division
            The Samuel Roberts Noble Foundation
            2510 Sam Noble Parkway, Ardmore, OK 73402, USA
            Tel: 580 224 6650
            Fax: 580 224 6692
            Email: gdmay@noble.org.
FEATURES             Location/Qualifiers
     source          1. .427
                     /organism="Medicago sativa"
                     /mol_type="mRNA"
                     /db_xref="taxon:3879"
                     /tissue_type="Glandular trichomes isolated from stem"
                     /dev_stage="Trichomes were removed from internodes of 8-12
                     inch tall stems"
                     /clone_lib="Glandular trichomes"
                     /note="Vector: pDNR-LIB; Glandular-haired alfalfa plants
                     were established in a Conviron growth chamber (16-h days,
                     full lights, 24oC set point) in 40 one gallon pots. Plants
```

were grown in Metromix 350 and fertilized with MiracleGro as needed. They were cut back closely to encourage the emergence of vigorous shoots. Trichomes were isolated from stems, approximately 8-12 inches long, clipped from plants 2-3 inches above the crown. With minimal handling of the stem, the apical bud, leaves and nodes were discarded, and the trichomes isolated from the internode segments."

ORIGIN

Query Match 78.2%; Score 17.2; DB 7; Length 427;
Best Local Similarity 86.4%; Pred. No. 6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||| ||||||| ||| ||||||
Db        198 TGATTGTGAACCTTCAAGATGA 177
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RESULT 13
AU083559
LOCUS AU083559 463 bp mRNA linear EST 02-APR-2002
DEFINITION AU083559 Rice green shoot Oryza sativa (japonica cultivar-group) cDNA clone S14862, mRNA sequence.
ACCESSION AU083559
VERSION AU083559.1 GI:7274015
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 463)
AUTHORS Sasaki,T. and Yamamoto,K.
TITLE Rice cDNA from green shoot (2000)
JOURNAL Unpublished (2000)
COMMENT Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
PROJECT ='RGP'.
FEATURES Location/Qualifiers
source 1. .463
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="S14862"
/clone_lib="Rice green shoot"
/note="Green shoot (8 days old)"

ORIGIN

Query Match 78.2%; Score 17.2; DB 1; Length 463;
Best Local Similarity 86.4%; Pred. No. 6.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||| ||||||| ||| ||||||
Db        151 TGAGTGTGAATGTTAGAGATGA 172
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RESULT 14
AU089685
LOCUS AU089685 479 bp mRNA linear EST 02-APR-2002
DEFINITION AU089685 Rice callus Oryza sativa (japonica cultivar-group) cDNA clone C40060, mRNA sequence.
ACCESSION AU089685
VERSION AU089685.1 GI:7652165
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 479)
AUTHORS Sasaki,T. and Yamamoto,K.
TITLE Rice cDNA from callus (2000)
JOURNAL Unpublished (2000)
COMMENT Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
PROJECT ='RGP'.
FEATURES Location/Qualifiers
source 1. .479
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="C40060"
/clone_lib="Rice callus"
/note="Vector: pBluescript II SK+; Site_1: SalI; Site_2: NotI; cDNA prepared from rice callus mRNAs by using oligo(dT) as a primer and ligating to the SalI-NotI site of pBluescript II SK+ phagemid. "

ORIGIN

Query Match 78.2%; Score 17.2; DB 1; Length 479;
Best Local Similarity 86.4%; Pred. No. 6.2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          1 TGACTGTGAACGTTCGAGATGA 22
              ||| ||||||| ||| ||||||
Db        299 TGAGTGTGAATGTTAGAGATGA 320
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RESULT 15
BJ094274
LOCUS BJ094274 513 bp mRNA linear EST 01-OCT-2003
DEFINITION BJ094274 NIBB Mochii normalized Xenopus early gastrula library Xenopus laevis cDNA clone XL144p18 5', mRNA sequence.
ACCESSION BJ094274
VERSION BJ094274.1 GI:17594227
KEYWORDS EST.
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Xenopus.
REFERENCE 1 (bases 1 to 513)
AUTHORS Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara,Y.
TITLE Expressed genes in X. laevis embryo
JOURNAL Unpublished (2001)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp
The information of this clone is available through the following URL.
http://xenopus.nibb.ac.jp.
FEATURES Location/Qualifiers
source 1. .513
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL144p18"
/tissue_type="whole embryo"

/dev_stage="stage 10.5"
/clone_lib="NIBB Mochii normalized Xenopus early gastrula library"
ORIGIN

Query Match 78.2%; Score 17.2; DB 4; Length 513;
Best Local Similarity 86.4%; Pred. No. 6.2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          1 TGACTGTGAACGTTCGAGATGA 22
              || ||| ||||||||| |||||
Db        198 TGCCTGAGAACGTTCGCGATGA 219
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Search completed: March 28, 2005, 23:50:21
Job time : 1998 secs